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Application No. 10/535,164

Docket No. 050992.0200.13USPC

AMENDMENTS TO THE SPECIFICATION

Between the title and the section heading "FIELD OF THE INVENTION," please remove the section heading "BACKGROUND OF THE INVENTION."

After the section entitled "CROSS REFERENCES TO RELATED APPLICATIONS," which was added at page 1 of the specification in the amendment filed on September 19, 2005, please replace the section heading "DESCRIPTION OF PRIOR ART" with the section heading "BACKGROUND OF THE INVENTION."

Please replace the paragraph at page 2, lines 16 through 20 with the following paragraph:

Sequence listing comprising 548,156 genomic sequences, is filed under section 801(a)(i) on electronic medium in computer readable form, attached to the present invention, and is hereby incorporated by reference. Said sequence listing is contained in ~~a self extracting compressed file named SEQ_LIST.EXE (9,813KB). Compressed file contains 1 file named SEQ_LIST.TXT (82,859KB) the file named "Patent12_Human_PCT_PatentIn_1.txt" (79,122 KB), which was created on June 4, 2008.~~

Please replace the paragraph at page 7, lines 21-23 with the following paragraph:

Figs. 2, 3, and 4 are schematic diagrams which when taken together provide an analogy that illustrates a conceptual model of the present invention, addressing the genomic differentiation engine. Fig. 2A depicts an analogy for gene expression. Fig. 2B depicts an analogy for differential gene expression between cells.

Please replace the paragraph at page 10, lines 7 and 8 with the following paragraph:

Fig. 23B is a schematic representation of secondary folding of hairpins of the operon-like cluster of Fig. 23A. The hairpins are associated with the following SEQ ID NOS: N2 (SEQ ID NO: 548172); N3 (SEQ ID NO: 548173); MIR23 (SEQ ID NO: 548174); GAM22 (SEQ ID NO: 548175); GAM116 (SEQ ID NO: 548176); N4 (SEQ ID NO: 548177); N6 (SEQ ID NO: 548178); MIR24 (SEQ ID NO: 548179); N7 (SEQ ID NO: 548180);

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Please replace the paragraph at page 10, lines 14-~~17~~ with the following paragraph:

Fig. 24A is an annotated sequence of EST72223 (SEQ ID NO: 548181) comprising known miRNA gene MIR98 and novel gene GAM25, both detected by the gene detection system of the present invention. The

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sequence of EST 72223 includes the four marked sequences: The sequence of the miRNA-98 hairpin in bold (SEQ ID NO: 548182), the sequence of the mature miRNA-98 in bold and underlined (SEQ ID NO: 548183), the sequence of the GAM25 hairpin in bold (SEQ ID NO: 548184) and the sequence of the mature miRNA of GAM25 in bold and underlined (SEQ ID NO: 548185).

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Please replace the paragraph at page 22, lines 5-8 with the following paragraph:

Finally, wet lab experiments are preferably conducted in order to validate expression and preferably function of the sample novel genes detected by the BIOINFORMATIC GENE DETECTION ENGINE 100 in the previous step, as designated by reference numeral 132. An example of wet-lab validation of the above mentioned sample novel gene bioinformatically detected by the system is described hereinbelow with reference to Figs. 22A and 22B.

Please replace the paragraphs at page 37, line 30 through page 38, line 24 with the following paragraphs:

First, genes of the novel group of genes of the present invention, referred to here as GAM genes, as designated by reference numeral 146, are located and their function elicited by detecting target proteins they bind and the function of those target proteins, as described hereinabove with reference to Figs. 9 through 15.

Next, genes of a novel group of operon-like genes of the present invention, referred to here as GR genes, as designated by reference numeral 147, are located, by locating clusters of proximally located GAM genes, based on the previous step.

Consequently, the hierarchy of GR and GAM genes is elicited, as designated by reference numeral 148: binding sites for non-protein-binding GAM genes comprised in each GR gene found are sought adjacent to other GR genes. When found, such a binding site indicates that the connection between the GAM and the GR the expression of which it modulates, and thus the hierarchy of the GR genes and the GAM genes they comprise.

Lastly, the function of GR genes and GAM genes which are 'high' in the hierarchy, i.e. GAM genes which modulate expression of other GR genes rather than directly modulating expression of target proteins, may be deduced. A preferred approach is as follows: The function of protein-modulating GAM genes is deducible from the protein which they modulate, provided that the function of these target proteins is known. The function of 'higher' GAM genes may be deduced by comparing the function of protein-modulating GAM genes, as designated by reference numeral 149, with the hierarchical relationships by which the 'higher' GAM genes are connected of the protein-modulating GAM genes. For example, given a group of several protein-modulating GAM genes, which collectively cause a protein expression pattern typical of a certain